AGGRESSIVENESS AND GENETIC VARIABILITY OF ROOT-KNOT NEMATODE *MELOIDOGYNE INCOGNITA* POPULATIONS IN COTTON (*GOSSYPIUM* SPP.) (Agresividad y variabilidad genética de poblaciones del nematodo agallador (*Meloidogyne incognita*) en algodón (*Gossypium* spp.).

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The root-knot nematode *Meloidogyne incognita* (Kofoid & White, 1919) Chitwood, 1949 is widely distributed and recognized as a major pathogen of cotton crop (*Gossypium* spp.) in Brazil. The objectives of this study were to assess the genetic variability and variation in aggressiveness among populations of *M. incognita* in cotton. Five isolates of *M. incognita*, esterases (Est I1 Rm 1.0 and Est I2 Rm 1.05 and 1.1) and one isolate of *Meloidogyne enterolobii* (an outgroup) were used in the analyses. DNA amplifications were done using 22 RAPD, 9 ISSR and 13 AFLP primers and cluster analyses were done using UPGMA. Our results showed that only 2.7% of the fragments were polymorphic. Despite the existence of two races (race 3 and 4) and two esterase phenotypes (I1 and I2), a low genetic variability among isolates was observed and this might be due to their mitotic parthenogenetic mode of reproduction. The aggressiveness of isolates to different cotton genotypes was also studied. The experiment was conducted under greenhouse conditions in which eight cotton cultivars were inoculated with 10.000 eggs per plant with each isolate. Four months post inoculation, nematode reproduction factor (RF) was determined. None of the populations was pathogenic to the cotton resistant genotypes M-315, TX -25, Semi Áspero Huanuco, Wild Mexican Jack Jones and CIR1348. Two populations of *M. incognita* from the states of Mato Grosso and Bahia, Brazil, were highly aggressive to the moderate resistant accessions La-887 and Clevewilt-6.

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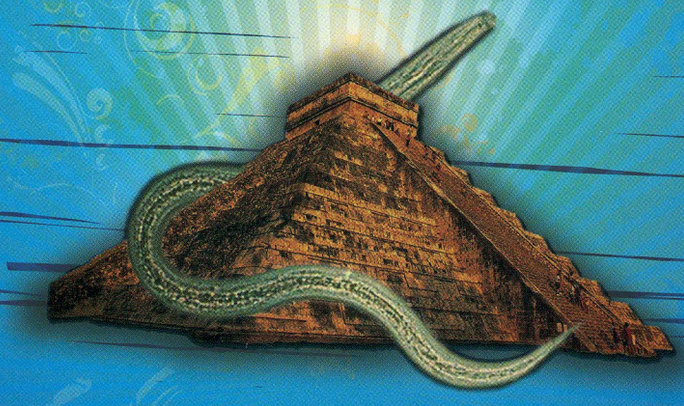
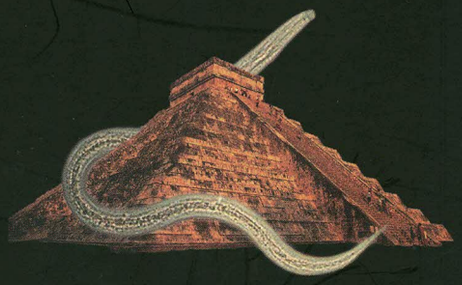


ABSTRACT BOOK



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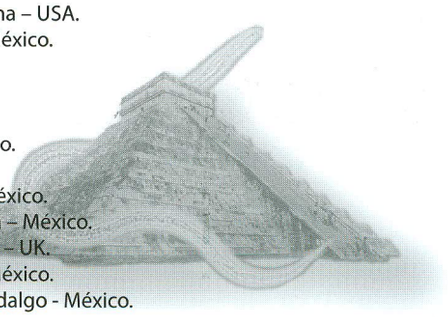

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